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<input type="checkbox"/>	L10	('6743599')!.PN.	2

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11/08/04

Search Results - Record(s) 1 through 2 of 2 returned.

L10: Entry 1 of 2

File: USPT

Jun 1, 2004

US-PAT-NO: 6743599

DOCUMENT-IDENTIFIER: US 6743599 B1

TITLE: Compositions and assays utilizing ADP or phosphate for detecting protein modulators

DATE-ISSUED: June 1, 2004

US-CL-CURRENT: 435/21; 435/15, 435/16, 435/17, 435/18, 435/19, 435/196, 435/23, 435/24INT-CL: [07] C12 Q 1/42, C12 Q 1/48, C12 Q 1/52, C12 Q 1/50, C12 N 9/18

L10: Entry 2 of 2

File: DWPI

Jun 1, 2004

DERWENT-ACC-NO: 2004-438685

ABSTRACTED-PUB-NO: US 6743599B

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TITLE: Identifying a compound that modulates polymerization or depolymerization of a cytoskeletal filament protein containing actin or tubulin involves use of adenosine diphosphate or phosphate

INT-CL (IPC): C12 N 9/18, C12 Q 1/42, C12 Q 1/48, C12 Q 1/50, C12 Q 1/52

Derwent-CL (DC): B04, D16

CPI Codes: B04-H20C1; B04-H20C2; B04-L01; B11-C10A; B12-K04E; B14-L01; B14-L06; D05-C03; D05-H09;

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L9: Entry 4 of 36

File: PGPB

Apr 1, 2004

DOCUMENT-IDENTIFIER: US 20040063097 A1

TITLE: Nanomachine compositions and methods of use

Detail Description Table CWU:

MG325 Ribosomal prt L33 0367 ribosomal protein L33 rpmG MG361 Ribosomal prt L10 0060 Ribosomal protein L10 rplJ MG362 Ribosomal prt L7/L12 0061 Ribosomal protein L7/L12 rplL P05387 (Human) MG363 Ribosomal prt L32 1292 Ribosomal protein L32 rpmF MG363a Ribosomal prt S20 0381 30S ribosomal protein S20 rpsT MG417 Ribosomal prt S9 0847 30S ribosomal protein S9 rpsI CAA21965 (Candida) MG418 Ribosomal prt L13 0848 Ribosomal protein L13 rplM P39473 (Sulfolobus) MG424 Ribosomal prt S15 0732 Ribosomal protein S15 rpsO CAC37508 (Schizosaccharomyces) MG426 Ribosomal prt L28 0368 Ribosomal protein L28 rpmB MG444 Ribosomal prt L19 1335 Ribosomal protein L19 rplS MG446 Ribosomal prt S16 1338 30S ribosomal protein S16 rpsP U33335 (Saccharomyces) MG466 Ribosomal prt L34 0415 50S ribosomal protein L34 rpmH Aerobic Metabolism MG102 Thioredoxin reductase 0570 Thioredoxin trxB NP_010640 (Saccharomyces) MG124 Thioredoxin 1221 Thioredoxin trxA P38141 (Saccharomyces) MG145 FAD synthase 0379 Nucleotidyltransferase yaaC NP_010522 (Saccharomyces) MG275 NADH Oxidase lpdP P09623 (Sus) MG398 ATP Synthase epsilon chain 1603 ATP synthase F1 epsilon subunit atpC MG399 ATP Synthase beta chain 1604 H⁺-transporting ATPase beta-subunit atpD P48413 (Cyanidium) MG400 ATP Synthase gamma chain 1605 ATP synthase F1 gamma subunit atpG MG401 ATP Synthase alpha chain 1606 ATP synthase F1 alpha subunit atpA P48413 (Cyanidium) MG402 ATP Synthase delta chain 1607 ATP synthase F1 delta subunit atpH MG403 ATP Synthase B chain 1608 ATP synthase F0 subunit b atpF MG404 ATP Synthase C chain 1609 H⁺-transporting ATP synthase C chain atpE MG405 Adenosinetriphosphatase 1610 ATP synthase F0 subunit a atpB MG408 peptide methionine sulfoxide reductase msrA NP_010960 (Saccharomyces) Glycolysis, Pyruvate Dehydrogenase & Pentose Phosphate Pathways MG023 Fructose-bisphosphate aldolase gatY P14540 (Saccharomyces) MG063 1-phosphofructokinase 1573 1-phosphofructokinase fruK P25332 (Saccharomyces) MG066 Transketolase 1 (TK 1) 0439 Transketolase 2 tkt P23254 (Saccharomyces) MG069 Phosphotransferase enzyme IIABC.sub.-- crr S74697 (Synechocystis) MG111 Phosphoglucose isomerase B 0973 Glucose-6-phosphate isomerase pgi NP_009755 (Saccharomyces) MG215 6-phosphofructokinase 0400 6-phosphofructokinase pfkA P16861 (Saccharomyces) MG216 Pyruvate kinase 0970 Pyruvate kinase pykA NP_014992 (Saccharomyces) MG271 Dihydrolipoamide Dehydrogenase 0640 Dihydrolipoamide dehydrogenase lpd P09624 (Saccharomyces) MG272 Dihydrolipoamide acetyltransferase 0641 Dihydrolipoamide acetyltransferase E2 aceF P10515 (Human) component MG273 Pyruvate Dehydrogenase E-1beta sub U09137 (Arabidopsis) MG274 Pyruvate Dehydrogenase E-1alpha sub NP_000047 (Human) MG300 Phosphoglycerate kinase 1647 Phosphoglycerate kinase pgk Q27685 (Leishmania) MG301 Glyceraldehyde 3-phosphate 1138 Glyceraldehyde 3-phosphate gapA P00359 (Saccharomyces) dehydrogenase dehydrogenase MG407 Enolase 0348 Enolase eno U09194 (Mesembryanthemum) MG430 Phosphoglycerate mutase yibO NP_013374 (Saccharomyces) MG431 Triosephosphate isomerase 0096 Triosephosphate isomerase tpiA Q07412 (Plasmodium) Carbohydrate Metabolism MG050 deoxyribose-phosphate aldolase 0528 Deoxyribose-phosphate aldolase deoC AAK68302 (Caenorhabditis) MG053 phosphomannomutase 0740 Phosphomannomutase yhbF NP_014005 (Saccharomyces) MG112 D-ribose-5-phosphate 3 epimerase 1370 Lytic transglycosylase yfhD NP_012414 (Saccharomyces) Central Intermediary Metabolism MG013 5,10-methylene-tetrahydrofolate 0027 5,10-methylene-tetrahydrofolate fold Q04448 (Drosophila)

dehydrogenase dehydrogenase MG038 Glycerol kinase 0108 Glycerol kinase glpK S36175 (Human) MG047 S-adenosylmethionine synthetase 0584 S-adenosylmethionine synthetase II metX NP_013281 (Saccharomyces) MG222 SAM-dependent methyltransferase 0542 SAM-dependent methyltransferase yabC MG228 Dihydrofolate reductase 0316 Dihydrofolate reductase folA U03885 (Paramecium) MG245 5,10-methenyltetrahydrofolate synthase 0275 0275 5-formyltetrahydrofolate cyclo-ligase ygfA P11586 (Human) MG293 Glycerophosphoryl diester 0106 Glycerophosphoryl diester glpQ phosphodiesterase phosphodiesterase MG299 Phosphotransacetylase 0612 Phosphotransacetylase ptap P38503 P38503 (Methanosarcina) MG347 SAM-dependent methyltransferase 1469 SAM-dependent methyltransferase yggH MG351 Inorganic pyrophosphatase 1555 Inorganic Pyrophosphatase Ppap/ppa P28239 (Saccharomyces) MG357 Acetate kinase 0613 Acetate kinase ackA MG380 SAM-dependent methyltransferase 1611 Glucose-inhibited division protein, gidB P38892 (Saccharomyces) methyltransferase MG394 Serine hydroxymethyltransferase (folate 0306 Serine hydroxymethyltransferase glyA P37291 (Saccharomyces) cycle) Nucleotide Metabolism: Purines, Pyrimidines, Nucleosides, and Nucleotides MG006 Thymidylate kinase 1582 Pyrimidine kinase ycfg AAC73211 (Human) MG030 Uracil Phosphoribosyltransferase 0637 Uracil phosphoribosyl transferase transferase upp U10246 (Toxoplasma) MG049 Purine-nucleoside phosphorylase 1640 Purine-nucleoside phosphorylase deoD BC003788 (Mus) MG052 Cytidine deaminase 0753 Cytidine deaminase Cddp/cdd P32320 (Human) MG058 Phosphoribosylpyrophosphate Synthase Synthase 1002 Ribose-phosphate pyrophosphokinase prsA P38689 (Saccharomyces) MG107 5'-guanylate kinase 1137 Guanylate kinase gmk KIBYGU (Saccharomyces) MG118 UDP-glucose 4-epimerase 1480 UDP-glucose 4-epimerase gale P04397 (Saccharomyces) MG171 Adenylate kinase 1478 Adenylate kinase adk P26364 (Saccharomyces) MG227 Thymidylate Synthase 0321 Thymidylate Synthase thyA U03885 (Paramecium) MG229 Ribonucleotide Reductase 2 1054 Ribonucleoside-diphosphate reductase, nrdB P42170 (Caenorhabditis) beta chain MG231 Ribonucleoside-diphosphate Reductase 1053 Ribonucleoside-diphosphate reductase nrdA CAB72517 (Campylobacter) MG268 Deoxyguano-deoxyadeno kinase (I) sub 2 MG276 Adenine Phosphoribosyltransferase 0639 Adenine phosphoribosyltransferase apt TAU22442 (Triticum) MG330 Cytidylate kinase 0628 Cytidylate kinase cmk U10120 (Mus) MG382 Uridine kinase 1266 Uridine kinase udk L31784 (Mus) MG434 uridylate kinase 0479 Uridine 5'-monophosphate kinase pyrH P37142 P37142 (Daucus) MG453 UDP-glucose pyrophosphorylase 0229 Glucosephosphate uridylyltransferase galU P32501 (Saccharomyces) MG458 Hypoxanthine-guanine 0565 Hypoxanthine phosphoribosyltransferase hpt P00492 (Human) Phosphoribosyltrnsfrse Regulatory Functions MG024 GTPase 1520 GTPase ychF P38746 (Saccharomyces)

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L9: Entry 12 of 36

File: PGPB

Sep 25, 2003

DOCUMENT-IDENTIFIER: US 20030180330 A1

TITLE: Method for identifying helicobacter antigens

Detail Description Table CWU:

TABLE 1 Systematic assignment of the proteins identified from H. pylori 26695. Proteins of Helicobacter pylori 26695 were separated by 2-DE. The protein spots were identified by PMF using MALDI-mass spectrometry. The proteins were grouped according to the protein classification described in Tomb et. al. (Nature 388: 539-547, 1997), which is deduced from the Echerichia coli gene classification of Riley (Microbiol. Rev. 57, 862-952, 1993). The number in brackets after each category refer to the total number of protein classification described in numbers were taken from TIGR database (Nov 24.sup.th 1999) (<http://www.tigr.org/tdb/>). NCBI Short Spot

No AccNo Protein name TIGR name ORF A Amino acid biosynthesis (44) A 1. Aromatic amino acid family (14) A 2. Aspartate family (14) B185 2313754

Tetrahydrodipicolinate N- DapD HP0626 succinyltransferase A 3. Glutamate family (3) A431 2494748 Glutamine synthetase GlnA HP0512 A 4. Pyruvate family (3) B192 3024012 Branched-chain-amino-acid IIve HP1468 aminotransferase A 5. Serine family (9) D3 2313177 Phosphoglycerate dehydrogenase -- HP0096 A 6. Other (1) B377 2313818

Hydantoin utilization protein A HyuA HP0695 B Purines, pyrimidines, nucleosides, and nucleotides (38) B 1. 2'-Deoxyribonucleotide metabolism (5) C186 3024765

Thioredoxin reductase TrxB HP0825 B 2. Purine ribonucleotide biosynthesis (12) F50 2498068 Nucleoside diphosphate kinase Ndk HP0198 C89 2497478 Adenylate kinase Adk HP0618 B488 2497358 Inosine-5'-monophosphate GuaB HP0829 dehydrogenase B 3. Pyrimidine ribonucleotide biosynthesis (11) B 4. Salvage of nucleosides and nucleotides (5) B403 2313187 2',3'-cyclic-nucleotide 2'- CpdB HP0104

phosphodiesterase B 5. Sugar-nucleotide biosynthesis and conversions (4) B 6. Other (1) C Fatty acid and phospholipid metabolism (26) C 1. Biosynthesis (24) D69 2313282 Enoyl-(acyl-carrier-protein) FabI HP0195 reductase (NADH) D295 2313678 3-ketoacyl-acyl carrier protein FabG HP0561 reductase B224 2313814 Acetyl coenzyme A FadA HP0690 acetyltransferase (thiolase) D96 2314546 3R)-hydroxymyristoyl-(acyl FabZ HP1376 carrier protein) dehydratase C 2. Degradation (2) D Biosynthesis of cofactors, prosthetic groups, and carriers (62) D 1. Biotin (7) D 2. Folic acid (7) D 3. Heme and porphyrin, and cobalamin (10) D 4. Menaquinone and ubiquinone (3) D 5. Molybdopterin (12) D 6. Pantothenate (4) D 7. Pyridoxine (2) D314 2314765

Pyridoxal phosphate biosynthetic PdxJ HP1582 protein J D 8. Riboflavin, FMN. and FAD (6) D 9. Glutathione (1) B321 2314270 Gamma-glutamyltranspeptidase Ggt HP1118 D 10. Thiamine (4) D 11. Pyridine nucleotides (3) D 12. Other (3) E Central intermediary metabolism (34) E 1. Amino sugars (1) E 2. Phosphorus compounds (3) C195 2500043 Inorganic pyrophosphatase Ppa HP0620 E 3. Polyamine biosynthesis (3) E 4. Other (27) C55 2507528 Urease accessory protein UreG HP0068 D84 2507527 Urease accessory protein UreF HP0069 D215 2507525 Urease accessory protein UreE HP0070

A343 137076 Urease beta subunit (urea UreB HP0072 amidohydrolase) A325 137076 Urease beta subunit (urea UreB HP0072 amidohydrolase) A323 137076 Urease beta subunit (urea UreB HP0072 amidohydrolase) D322 137069 Urease, alpha subunit UreA HP0073 D318 137069 Urease, alpha subunit UreA HP0073 D316 137069 Urease, alpha subunit UreA HP0073 D323 137069 Urease, alpha subunit UreA HP0073 D326 130769 Urease, alpha subunit UreA HP0073 C109 2314035 Hydrogenase HypB HP0900

expression/formation protein D200 2314346 Carbonic anhydrase -- HP1186 F Energy metabolism (108) F 1. Aerobic (15) F 2. Amino acids and amines (8) B511 2313392

Aliphatic amidase Aime HP0294 F 3. Anaerobic (11) B17 2494617 Fumarate reductase, flavoprotein FrdA HP0192 subunit B516 2313707 Ferredoxin oxidoreductase, -- HP0589 alpha subunit D287 2314259 Pyruvate ferredoxin -- HP1108 oxidoreductase, gamma subunit D188 2314262 Pyruvate ferredoxin -- HP1111 oxidoreductase, beta subunit 2565251 F 4. ATP-proton motive force interconversion (9) A209 2197129 ATP synthase F1, subunit beta AtpD HP1132 B465 2493030 ATP synthase F1, subunit AtpG HP1133 gamma gamma F 5. Electron transport (29) E41 3024719 Thioredoxin TrxA HP0824 E59 3024719 Thioredoxin TrxA HP0824 E29 3024719 Thioredoxin TrxA HP0824 D230 2314091 Oxygen-insensitive NAD(P)H -- HP0954 nitroreductase E62 2314319 Flavodoxin FldA HP1161 E60 2314319 Flavodoxin FldA HP1161 B480 2314321 Thioredoxin reductase TrxB HP1164 F34 2314636 Thioredoxin -- HP1458 D236 2314722 Ubiquinol cytochrome c FbcF HP1540 oxidoreductase, Rieske 2Fe-2S subunit F 6. Entner-Doudoroff (2) F 7. Fermentation (6) C155 2492992 3-oxoadipate coA-transferase YxjD HP0691 subunit A C110 2492996 3-oxoadipate coA-transferase YxjE HP0692 subunit B F 8. Glycolysis/gluconeogenesis (14) A487 2506387 Enolase Eno HP0154 D7 2492813 Fructose-bisphosphate aldolase Tsr HP0176 F 9. Pentose phosphate pathway (5) F 10. Sugars (2) B173 2313462 UDP-glucose 4-epimerase -- HP0360 F 11. TCA cycle (5) B483 2493711 Citrate synthase GltA HP0026 B492 2497255 Isocitrate dehydrogenase Icd HP0027 B499 2497255 Isocitrate dehydrogenase Icd HP0027 B210 2497255 Isocitrate dehydrogenase Icd HP0027 B2 3023247 Aconitase B AcnB HP0779 B505 2314492 Fumarase FumC HP1325 F 12. Other (2) G Transport and binding proteins (119) G 1. Amino acids, peptides and amines (29) D174 2313399 Dipeptide ABC transporter, DppD HP0301 ATP-binding protein G 2. Anions (5) G 3. Carbohydrates, organic alcohols, and acids (6) G 4. Cations (24) D221 2314745 Iron(III) ABC transporter, CeuE HP1561 periplasmic iron-binding protein D313 2314746 Iron(III) ABC transporter, CeuE HP1562 periplasmic iron-binding protein G 5. Nucleosides, purines and pyrimidines (2) G 6. Other (15) G 7. Unknown substrate (38) H DNA metabolism (105) H 1. DNA replication, recombination, and repair (54) H 2. Restriction/modification (48) H 3. Degradation of DNA (2) H 4. Chromosome-associated proteins (1) D180 2314294 Plasmid replication-partition -- HP1138 related protein I Transcription (10) I 1. Degradation of RNA (1) I 2. DNA-dependent RNA polymerase (2) A461 2500600 DNA-directed RNA polymerase, RpoA HP1293 alpha subunit I 3. Transcription factors (4) C69 2494920 Transcription elongation factor GreA HP0866 GreA D93 2499340 Transcription termination factor NusG HP1203 NusG I 4. RNA processing (3) J Protein synthesis (99) J 1. tRNA aminoacylation (26) J 2.

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Jun 1, 2004

TITLE: Compositions and assays utilizing ADP or phosphate for detecting protein modulators

In a preferred embodiment, the target protein directly produces ADP or phosphate. In a preferred embodiment, the target protein is an enzyme having activity which produces ADP and/or phosphate as a reaction product. For example, proteins which directly produce ADP include but are not limited to ATPases, kinases, GTPases, phosphatases and phosphorylases. Suitable ATPases include, but are not limited to, myosins, kinesins, dyneins, DNA gyrase, DNA helicase, topoisomerase I and II, Na⁺-K⁺ ATPase, Ca²⁺ ATPase, F1 subunit of ATP synthase, terminase/DNA packaging protein; protein; recA, heat shock proteins, NSF, katanin, SecA, 5-lipoxygenase, and actin. Suitable kinases include, but are not limited to, tyrosine kinases; serine-threonine kinases; receptor tyrosine kinases; growth factor receptors including but not limited to insulin receptor, epidermal growth factor receptor, platelet derived growth factor receptor and fibroblast growth factor receptor; ErbB2; calmodulin dependent protein kinases; protein kinase A; protein kinase C; myosin light chain kinase; CDK2 kinase; ROCK1 kinases; Src kinases; phosphorylase kinase; CheA; adenylate kinase; glycolytic kinases; EIF-2 alpha protein kinases; and Abl. Suitable GTPases include, but are not limited to, G proteins, Rho family GTPases: cdc42, RalA, RhoA and Rac1; Ras proteins; elongation factors including EF1.alpha., EF1.beta..gamma., EF-Tu and EF-G; septins; tubulin; ARF related GTPase; rab; SSRP receptor; rhodopsin; transducin; and GTPase activating protein (GAP). Suitable phosphatases include, but are not limited to, protein phosphatases; myosin phosphatase; IP3 phosphatase; pyrophosphatase; and Cdc25. Suitable phosphorylases include, but are not limited to, polynucleotide phosphorylase and glycogen phosphorylase.

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Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name **ATPG_PASMU**
 Primary accession number **Q9L6B6**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 40, October 2001
 Sequence was last modified in Release 40, October 2001
 Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **ATP synthase gamma chain**
 Synonym **EC 3.6.3.14**
 Gene name **Name: atpG**
 OrderedLocusNames: **PM1493**
 From **Pasteurella multocida [TaxID: 747]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

Fuller T.E., Kennedy M.J., Lowery D.E.;

"Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Pm70;

DOI=[10.1073/pnas.051634598](#);MEDLINE=21145866;PubMed=11248100 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

[Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465\(2001\).](#)

Comments

- **FUNCTION:** Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- **CATALYTIC ACTIVITY:** $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.
- **SUBUNIT:** F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
- **SIMILARITY:** Belongs to the ATPase gamma chain family.

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Cross-references

EMBL	AF237922; AAF68408.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE006186; AAK03577.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P00837; 1FS0. [HSSP ENTRY / PDB]
CMR	Q9L6B6 ; PM1493.
InterPro	IPR000131 ; ATPase_gamma. Graphical view of domain structure .
Pfam	PF00231 ; ATP-synt; 1. Pfam graphical view of domain structure .
PRINTS	PR00126 ; ATPASEGAMMA.
TIGRFAMs	TIGR01146 ; ATPsyn_F1gamma; 1.
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ProtoMap	Q9L6B6 .
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ModBase	Q9L6B6 .
SMR	Q9L6B6 ; 1E1E862B4EEA9F70.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords

ATP synthesis; CF(1); Complete proteome; Hydrogen ion transport; Hydrolase.

Features

None

Sequence information

Length: 289 Molecular weight: 32095 CRC64: 1E1E862B4EEA9F70 [This is a checksum on the sequence]

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RA  May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT  "Complete genomic sequence of Pasteurella multocida, Pm70";
RL  Proc. Natl. Acad. Sci. U.S.A. 98(6):3460-3465(2001).
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RL  Submitted (24-OCT-2000) to the EMBL/GenBank/DDBJ databases.
RL  Department of Veterinary Pathobiology, University of Minnesota, 1971
RL  Commonwealth Ave., St. Paul, MN 55108, USA
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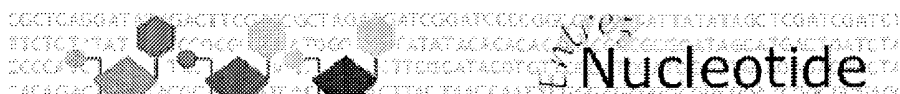
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 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
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 REFERENCE 2 (bases 1 to 10699)
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10681 aagtttaact tttggcaag
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//

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```

ID  AF237922  standard; genomic DNA; PRO; 870 BP.
XX
AC  AF237922;
XX
SV  AF237922.1
XX
DT  08-MAY-2000 (Rel. 63, Created)
DT  08-MAY-2000 (Rel. 63, Last updated, Version 1)
XX
DE  Pasteurella multocida ATP synthase F1 gamma chain (atpG) gene, complete
DE  cds.
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KW  .
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OS  Pasteurella multocida
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Pasteurella.
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RN  [1]
RP  1-870
RA  Fuller T.E., Kennedy M.J., Lowery D.E.;
RT  "Identification of Pasteurella multocida virulence genes in a septicemic
RT  mouse model using signature-tagged mutagenesis";
RL  Unpublished.
XX
RN  [2]
RP  1-870
RA  Fuller T.E., Kennedy M.J., Lowery D.E.;
RT  ;
RL  Submitted (24-FEB-2000) to the EMBL/GenBank/DDBJ databases.
RL  Discovery Research, Pharmacia & Upjohn Animal Health, 7923-25-434, 7000
RL  Portage Road, Kalamazoo, MI 49001-0199, USA
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Entry information

Entry name **ATPG_HAEIN**
 Primary accession number **P43716**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 32, November 1995
 Sequence was last modified in Release 32, November 1995
 Annotations were last modified in Release 45, October 2004

Name and origin of the protein

Protein name **ATP synthase gamma chain**
 Synonym **EC 3.6.3.14**
 Gene name **Name: atpG**
 OrderedLocusNames: **HI0480**
 From **Haemophilus influenzae [TaxID: 727]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; **PubMed**=7542800 [NCBI, ExPASy, EBI, Israel, Japan]
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., , Venter J.C.;
 "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; Science 269:496-512(1995).

Comments

- **FUNCTION:** Produces ATP from ADP in the presence of a proton gradient across the membrane. The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.
- **CATALYTIC ACTIVITY:** $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.

- **SUBUNIT:** F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
- **SIMILARITY:** Belongs to the ATPase gamma chain family.

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Cross-references

EMBL U32730; AAC22138.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 PIR E64071; E64071.
 HSSP P00837; 1FS0. [HSSP ENTRY / PDB]
 TIGR HI0480; -.
 InterPro IPR000131; ATPase_gamma.
 Graphical view of domain structure.
 Pfam PF00231; ATP-synt; 1.
 Pfam graphical view of domain structure.
 PRINTS PR00126; ATPASEGAMMA.
 TIGRFAMs TIGR01146; ATPsyn_F1gamma; 1.
 PROSITE PS00153; ATPASE_GAMMA; 1.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 BLOCKS P43716.
 ProtoNet P43716.
 ProtoMap P43716.
 PRESAGE P43716.
 DIP P43716.
 ModBase P43716.
 SMR P43716; 622CBA682F37FD00.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

ATP synthesis; CF(1); Complete proteome; Hydrogen ion transport; Hydrolase.

Features

None

Sequence information

Length: **289** Molecular weight: **32069** CRC64: **622CBA682F37FD00** [This is a checksum on the
 AA Da sequence]

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      |           |           |           |           |           |
QKPVVQQLVP LPESKDDHLN ERQQTWDYLY EPEPKVLLDS LLVRYLESQI YQAVVDNVA

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      |           |           |           |
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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.12 sec, SCORE=11730, Nseq=2, Len=289

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sp|P43716|ATPG_HAEIN          IGYKHPFLVEREVKKIGILVISTDRGMCGLNVLNLFKTTLNQIKNWKEQNISTDL
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CLUSTAL FORMAT for T-COFFEE Version 1.37, CPU=0.13 sec, SCORE=9860, Nseq=2, Len=289

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* : * * * * * : : : * : * * * * * : * : * * * * * : * : * * * * *
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sp|P00837|ATPG_ECOLI              QVPTISQLLPLPASDDDDL--KHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVV
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***** * **.******.*.* **.******.*
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<input type="checkbox"/>	sp	Q9K6H4	ATPG_BACHD ATP synthase gamma chain (EC 3.6.3.14) [atp...	208	8e-53
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<input type="checkbox"/>	tr	Q6HAX9	ATP synthase F1, gamma subunit (EC 3.6.3.14) [atpG] [B...	207	2e-52
<input type="checkbox"/>	tr	Q81JZ4	ATP synthase F1, gamma subunit [atpG] [Bacillus anthra...	207	2e-52
<input type="checkbox"/>	tr	Q814W1	ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bacil...	207	2e-52
<input type="checkbox"/>	tr	Q72XE7	ATP synthase F1, gamma subunit (EC 3.6.3.14) [atpG] [B...	207	2e-52
<input type="checkbox"/>	tr	Q630U2	ATP synthase F1, gamma subunit (EC 3.6.3.14) [atpG] [B...	207	2e-52
<input type="checkbox"/>	tr	Q8E5U9	H ⁺ -transporting ATP synthase gamma chain [atpG] [Strep...	205	8e-52
<input type="checkbox"/>	tr	Q831A4	ATP synthase F1, gamma subunit [atpG] [Enterococcus fa...	205	8e-52
<input type="checkbox"/>	tr	Q9RAU1	H ⁺ -ATPase cytoplasmic F1-part gamma-subunit [atpG] [La...	204	1e-51
<input type="checkbox"/>	tr	Q7DH73	H ⁺ -ATPase gamma subunit [atpG] [Lactococcus lactis (su...	204	1e-51
<input type="checkbox"/>	sp	Q9CER9	ATPG_LACLA ATP synthase gamma chain (EC 3.6.3.14) [atp...	204	2e-51
<input type="checkbox"/>	tr	Q8E073	ATP synthase F1, gamma subunit [atpG] [Streptococcus a...	202	4e-51
<input type="checkbox"/>	tr	Q65DX3	AtpG [atpG] [Bacillus licheniformis DSM 13]	202	7e-51
<input type="checkbox"/>	tr	O05432	ATP synthase subunit gamma [atpG] [Moorella thermoacet...	201	9e-51
<input type="checkbox"/>	tr	O50158	Proton-translocating ATPase, gamma subunit [atpG] [Str...	201	2e-50
<input type="checkbox"/>	tr	Q8EM82	H(+)-transporting ATP synthase gamma chain (EC 3.6.1.3...	197	1e-49
<input type="checkbox"/>	tr	Q7CND4	Putative proton-translocating ATPase, gamma subunit [a...	197	1e-49
<input type="checkbox"/>	tr	Q9A0I8	Putative proton-translocating ATPase, gamma subunit (E...	197	1e-49
<input type="checkbox"/>	sp	P09222	ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6....	196	3e-49
<input type="checkbox"/>	tr	Q8K827	Putative proton-translocating ATPase, gamma subunit [S...	196	3e-49
<input type="checkbox"/>	tr	Q7CRB2	Proton-translocating ATPase, F1 sector, gamma-subunit ...	196	4e-49
<input type="checkbox"/>	tr	Q97PT5	ATP synthase F1, gamma subunit (Proton-translocating A...	196	4e-49
<input type="checkbox"/>	tr	Q52412	TF1-gamma subunit [Bacillus PS3 (Thermophilic bacteriu...	196	5e-49
<input type="checkbox"/>	tr	Q6AQ11	Probable ATP synthase, gamma chain (AtpG) [DP0833] [De...	195	9e-49
<input type="checkbox"/>	tr	Q74GY1	ATP synthase F1, gamma subunit (EC 3.6.3.14) [atpG] [G...	194	1e-48
<input type="checkbox"/>	tr	Q8RKV3	H ⁺ -ATPase cytoplasmic F1-part gamma-subunit [atpG] [St...	194	2e-48
<input type="checkbox"/>	sp	P12408	ATPG_ANASP ATP synthase gamma chain (EC 3.6.3.14) [atp...	193	3e-48

<input type="checkbox"/>	tr	Q8CNJ6	ATP synthase gamma chain [SE1701] [Staphylococcus epid...	193	3e-48
<input type="checkbox"/>	tr	Q7MA19	ATP SYNTHASE F1 GAMMA SUBUNIT (EC 3.6.3.14) [ATPG] [Wo...	193	3e-48
<input type="checkbox"/>	tr	Q7ANV0	AtpG protein [atpG] [Listeria innocua]	193	3e-48
<input type="checkbox"/>	tr	Q71WP8	ATP synthase F1, gamma subunit (EC 3.6.3.14) [atpG] [L...	193	3e-48
<input type="checkbox"/>	tr	Q927W3	AtpG protein [atpG] [Listeria monocytogenes]	193	3e-48
<input type="checkbox"/>	sp	P17253	ATPG_SYNY3 ATP synthase gamma chain (EC 3.6.3.14) [atp...	192	6e-48
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<input type="checkbox"/>	tr	Q6G7K6	ATP synthase gamma chain (EC 3.6.3.14) [SAS2007] [Stap...	192	6e-48
<input type="checkbox"/>	tr	Q7A4E8	ATP synthase gamma chain [atpG] [Staphylococcus aureus...	192	6e-48
<input type="checkbox"/>	tr	Q7A0C5	ATP synthase gamma chain [atpG] [Staphylococcus aureus...	192	6e-48

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